

Paul M Thomas

List of Publications by Year in descending order

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121
papers

8,344
citations

38738

50
h-index

49904

87
g-index

126
all docs

126
docs citations

126
times ranked

9879
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.	27.8	587
2	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
3	The MMSET histone methyl transferase switches global histone methylation and alters gene expression in t(4;14) multiple myeloma cells. <i>Blood</i> , 2011, 117, 211-220.	1.4	300
4	Complete Protein Characterization Using Top-Down Mass Spectrometry and Ultraviolet Photodissociation. <i>Journal of the American Chemical Society</i> , 2013, 135, 12646-12651.	13.7	297
5	Loss of BAP1 function leads to EZH2-dependent transformation. <i>Nature Medicine</i> , 2015, 21, 1344-1349.	30.7	297
6	Discovery and in vitro biosynthesis of haloduracin, a two-component lantibiotic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17243-17248.	7.1	215
7	The vermiform appendix impacts the risk of developing Parkinson's disease. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	205
8	Deconstruction of Iterative Multidomain Polyketide Synthase Function. <i>Science</i> , 2008, 320, 243-246.	12.6	202
9	ProSight Lite: Graphical software to analyze top-down mass spectrometry data. <i>Proteomics</i> , 2015, 15, 1235-1238.	2.2	196
10	On the Scalability and Requirements of Whole Protein Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 6868-6874.	6.5	177
11	TRACKING ACIDIC PHARMACEUTICALS, CAFFEINE, AND TRICLOSAN THROUGH THE WASTEWATER TREATMENT PROCESS. <i>Environmental Toxicology and Chemistry</i> , 2005, 24, 25.	4.3	169
12	Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. <i>Nature Communications</i> , 2018, 9, 1203.	12.8	165
13	A scalable platform to identify fungal secondary metabolites and their gene clusters. <i>Nature Chemical Biology</i> , 2017, 13, 895-901.	8.0	154
14	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	2.2	147
15	Analysis of Intact Monoclonal Antibody IgG1 by Electron Transfer Dissociation Orbitrap FTMS. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1758-1767.	3.8	137
16	Large-scale Top-down Proteomics of the Human Proteome: Membrane Proteins, Mitochondria, and Senescence. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3465-3473.	3.8	132
17	Total kinetic analysis reveals how combinatorial methylation patterns are established on lysines 27 and 36 of histone H3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13549-13554.	7.1	129
18	Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. <i>Nature Chemical Biology</i> , 2007, 3, 480-485.	8.0	126

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19	A proteomics approach to discovering natural products and their biosynthetic pathways. <i>Nature Biotechnology</i> , 2009, 27, 951-956.	17.5	125
20	Diversity of Amyloid-beta Proteoforms in the Alzheimer's Disease Brain. <i>Scientific Reports</i> , 2017, 7, 9520.	3.3	125
21	Cover Picture: Proteomics 7'15. <i>Proteomics</i> , 2015, 15, NA-NA.	2.2	119
22	Heterologous Production of Fosfomycin and Identification of the Minimal Biosynthetic Gene Cluster. <i>Chemistry and Biology</i> , 2006, 13, 1171-1182.	6.0	116
23	Top-Down Proteomics on a Chromatographic Time Scale Using Linear Ion Trap Fourier Transform Hybrid Mass Spectrometers. <i>Analytical Chemistry</i> , 2007, 79, 7984-7991.	6.5	116
24	A protease for 'middle-down' proteomics. <i>Nature Methods</i> , 2012, 9, 822-824.	19.0	103
25	The biosynthesis of methanobactin. <i>Science</i> , 2018, 359, 1411-1416.	12.6	101
26	Measurement of acetylation turnover at distinct lysines in human histones identifies long-lived acetylation sites. <i>Nature Communications</i> , 2013, 4, 2203.	12.8	100
27	The emerging process of Top Down mass spectrometry for protein analysis: biomarkers, protein-therapeutics, and achieving high throughput. <i>Molecular BioSystems</i> , 2010, 6, 1532.	2.9	92
28	Size-Sorting Combined with Improved Nanocapillary Liquid Chromatography-Mass Spectrometry for Identification of Intact Proteins up to 80 kDa. <i>Analytical Chemistry</i> , 2010, 82, 1234-1244.	6.5	91
29	The first pilot project of the consortium for top-down proteomics: <scp>A</scp> status report. <i>Proteomics</i> , 2014, 14, 1130-1140.	2.2	90
30	The emergence of top-down proteomics in clinical research. <i>Genome Medicine</i> , 2013, 5, 53.	8.2	89
31	Cloning, Expression, and Biochemical Characterization of <i>Streptomyces rubellomurinus</i> Genes Required for Biosynthesis of Antimalarial Compound FR900098. <i>Chemistry and Biology</i> , 2008, 15, 765-770.	6.0	88
32	Applying Label-Free Quantitation to Top Down Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 4961-4968.	6.5	88
33	Evaluation of the Compact High-Field Orbitrap for Top-Down Proteomics of Human Cells. <i>Journal of Proteome Research</i> , 2012, 11, 4308-4314.	3.7	84
34	Ultraviolet Photodissociation for Characterization of Whole Proteins on a Chromatographic Time Scale. <i>Analytical Chemistry</i> , 2014, 86, 2185-2192.	6.5	81
35	Programmed Ribosomal Frameshifting Generates a Copper Transporter and a Copper Chaperone from the Same Gene. <i>Molecular Cell</i> , 2017, 65, 207-219.	9.7	81
36	Identification and Characterization of Human Proteoforms by Top-Down LC-21 Tesla FT-ICR Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 1087-1096.	3.7	81

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37	Expansion for the <i>Brachylophosaurus canadensis</i> Collagen I Sequence and Additional Evidence of the Preservation of Cretaceous Protein. <i>Journal of Proteome Research</i> , 2017, 16, 920-932.	3.7	80
38	The C-Score: A Bayesian Framework to Sharply Improve Proteoform Scoring in High-Throughput Top Down Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 3231-3240.	3.7	76
39	Fungal artificial chromosomes for mining of the fungal secondary metabolome. <i>BMC Genomics</i> , 2015, 16, 343.	2.8	76
40	Native top-down mass spectrometry provides insights into the copper centers of membrane-bound methane monooxygenase. <i>Nature Communications</i> , 2019, 10, 2675.	12.8	74
41	Top Down Proteomics of Human Membrane Proteins from Enriched Mitochondrial Fractions. <i>Analytical Chemistry</i> , 2013, 85, 1880-1888.	6.5	72
42	High-Throughput Analysis of Intact Human Proteins Using UVPD and HCD on an Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2017, 16, 2072-2079.	3.7	69
43	Integrated Bottom-Up and Top-Down Proteomics of Patient-Derived Breast Tumor Xenografts. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 45-56.	3.8	68
44	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. <i>Clinical Cancer Research</i> , 2019, 25, 222-239.	7.0	66
45	The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells. <i>Science</i> , 2022, 375, 411-418.	12.6	64
46	Robust Analysis of the Yeast Proteome under 50 kDa by Molecular-Mass-Based Fractionation and Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 209-215.	6.5	62
47	NMT1 and NMT2 are lysine myristoyltransferases regulating the ARF6 GTPase cycle. <i>Nature Communications</i> , 2020, 11, 1067.	12.8	62
48	Mass Spectrometry and Antibody-Based Characterization of Blood Vessels from <i>Brachylophosaurus canadensis</i> . <i>Journal of Proteome Research</i> , 2015, 14, 5252-5262.	3.7	59
49	A Highly Productive, One-Pot Cell-Free Protein Synthesis Platform Based on Genomically Recoded <i>Escherichia coli</i> . <i>Cell Chemical Biology</i> , 2019, 26, 1743-1754.e9.	5.2	59
50	Kinetics of Re-establishing H3K79 Methylation Marks in Global Human Chromatin*. <i>Journal of Biological Chemistry</i> , 2010, 285, 32778-32786.	3.4	56
51	Unabridged Analysis of Human Histone H3 by Differential Top-Down Mass Spectrometry Reveals Hypermethylated Proteoforms from MMSET/NSD2 Overexpression. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 776-790.	3.8	56
52	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019, 16, 939-940.	19.0	55
53	Determination of Nonsteroidal Anti-inflammatory Drugs, Caffeine, and Triclosan in Wastewater by Gas Chromatography-Mass Spectrometry. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2004, 39, 1969-1978.	1.7	54
54	Characterization of a long overlooked copper protein from methane- and ammonia-oxidizing bacteria. <i>Nature Communications</i> , 2018, 9, 4276.	12.8	46

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55	Microbial and metabolic succession on common building materials under high humidity conditions. <i>Nature Communications</i> , 2019, 10, 1767.	12.8	46
56	Developing top down proteomics to maximize proteome and sequence coverage from cells and tissues. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 787-794.	6.1	45
57	In Vitro Biosynthesis of Unnatural Enterocin and Wailupemycin Polyketides. <i>Journal of Natural Products</i> , 2009, 72, 469-472.	3.0	43
58	Deeper Protein Identification Using Field Asymmetric Ion Mobility Spectrometry in Top-Down Proteomics. <i>Analytical Chemistry</i> , 2021, 93, 6323-6328.	6.5	40
59	Reassignment of the Structure of the Antibiotic A53868 Reveals an Unusual Amino Dehydrophosphonic Acid. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 9089-9092.	13.8	38
60	Thorough Performance Evaluation of 213 nm Ultraviolet Photodissociation for Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 405-420.	3.8	38
61	Bone protein "extractomics" comparing the efficiency of bone protein extractions of <i>Gallus gallus</i> in tandem mass spectrometry, with an eye towards paleoproteomics. <i>PeerJ</i> , 2016, 4, e2603.	2.0	38
62	Top-Down Proteomics with Mass Spectrometry Imaging: A Pilot Study towards Discovery of Biomarkers for Neurodevelopmental Disorders. <i>PLoS ONE</i> , 2014, 9, e92831.	2.5	37
63	Proteoforms in Peripheral Blood Mononuclear Cells as Novel Rejection Biomarkers in Liver Transplant Recipients. <i>American Journal of Transplantation</i> , 2017, 17, 2458-2467.	4.7	37
64	Gatekeeping versus Promiscuity in the Early Stages of the Andrimid Biosynthetic Assembly Line. <i>ACS Chemical Biology</i> , 2008, 3, 542-554.	3.4	36
65	Determination of 5-Methyltetrahydrofolic Acid and Folic Acid in Citrus Juices Using Stable Isotope Dilution Mass Spectrometry. <i>Journal of Agricultural and Food Chemistry</i> , 2003, 51, 1293-1296.	5.2	35
66	Deciphering the Late Biosynthetic Steps of Antimalarial Compound FR-900098. <i>Chemistry and Biology</i> , 2010, 17, 57-64.	6.0	35
67	Deep and quantitative top-down proteomics in clinical and translational research. <i>Expert Review of Proteomics</i> , 2014, 11, 649-651.	3.0	35
68	The Value of Activated Ion Electron Transfer Dissociation for High-Throughput Top-Down Characterization of Intact Proteins. <i>Analytical Chemistry</i> , 2018, 90, 8553-8560.	6.5	35
69	The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. <i>Nature Cancer</i> , 2020, 1, 653-664.	13.2	35
70	Characterization of Methanobactin from <i>Methylosinus</i> sp. LW4. <i>Journal of the American Chemical Society</i> , 2016, 138, 11124-11127.	13.7	34
71	High-definition De Novo Sequencing of Crustacean Hyperglycemic Hormone (CHH)-family Neuropeptides. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1951-1964.	3.8	31
72	Site-specific human histone H3 methylation stability: fast K4me3 turnover. <i>Proteomics</i> , 2014, 14, 2190-2199.	2.2	30

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73	Identification of the First Diketomorpholine Biosynthetic Pathway Using FAC-MS Technology. ACS Chemical Biology, 2018, 13, 1142-1147.	3.4	30
74	A clinically relevant murine model unmasks a "two-hit" mechanism for reactivation and dissemination of cytomegalovirus after kidney transplant. American Journal of Transplantation, 2019, 19, 2421-2433.	4.7	28
75	Top-Down Proteomics Enables Comparative Analysis of Brain Proteoforms Between Mouse Strains. Analytical Chemistry, 2018, 90, 3802-3810.	6.5	27
76	Accurate Estimation of Context-Dependent False Discovery Rates in Top-Down Proteomics. Molecular and Cellular Proteomics, 2019, 18, 796-805.	3.8	27
77	Bioinformatics Analysis of Top-Down Mass Spectrometry Data with ProSight Lite. Methods in Molecular Biology, 2017, 1558, 381-394.	0.9	27
78	Identification and targeting of novel CDK9 complexes in acute myeloid leukemia. Blood, 2019, 133, 1171-1185.	1.4	26
79	Fragmentation of Integral Membrane Proteins in the Gas Phase. Analytical Chemistry, 2014, 86, 4627-4634.	6.5	25
80	Defining the Neuropeptidome of the Spiny Lobster <i>Panulirus interruptus</i> Brain Using a Multidimensional Mass Spectrometry-Based Platform. Journal of Proteome Research, 2015, 14, 4776-4791.	3.7	24
81	PAI-1 is a critical regulator of FGF23 homeostasis. Science Advances, 2017, 3, e1603259.	10.3	24
82	Comparative top down proteomics of peripheral blood mononuclear cells from kidney transplant recipients with normal kidney biopsies or acute rejection. Proteomics, 2016, 16, 2048-2058.	2.2	22
83	Proteome-Selective Imaging of Tissues Using Mass Spectrometry**. Angewandte Chemie - International Edition, 2022, 61, .	13.8	22
84	EphA2 proteomics in human keratinocytes reveals a novel association with afadin and epidermal tight junctions. Journal of Cell Science, 2017, 130, 111-118.	2.0	21
85	Mass spectral determinations of the folic acid content of fortified breads from Chile. Journal of Food Composition and Analysis, 2003, 16, 281-286.	3.9	20
86	Top Down Proteomics Reveals Mature Proteoforms Expressed in Subcellular Fractions of the <i>Echinococcus granulosus</i> Preadult Stage. Journal of Proteome Research, 2015, 14, 4805-4814.	3.7	19
87	Interrogation of Benzomalvin Biosynthesis Using Fungal Artificial Chromosomes with Metabolomic Scoring (FAC-MS): Discovery of a Benzodiazepine Synthase Activity. Biochemistry, 2018, 57, 3237-3243.	2.5	19
88	Histone tail analysis reveals H3K36me2 and H4K16ac as epigenetic signatures of diffuse intrinsic pontine glioma. Journal of Experimental and Clinical Cancer Research, 2020, 39, 261.	8.6	16
89	A synthetic biology approach to probing nucleosome symmetry. ELife, 2017, 6, .	6.0	16
90	The Human Proteoform Atlas: a FAIR community resource for experimentally derived proteoforms. Nucleic Acids Research, 2022, 50, D526-D533.	14.5	15

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91	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.	3.7	14
92	A mixed-valent Fe(II)Fe(III) species converts cysteine to an oxazolone/thioamide pair in methanobactin biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2123566119.	7.1	14
93	Multidimensional Top-Down Proteomics of Brain-Region-Specific Mouse Brain Proteoforms Responsive to Cocaine and Estradiol. <i>Journal of Proteome Research</i> , 2019, 18, 3999-4012.	3.7	12
94	Heterologous Expression of the Unusual Terreazepine Biosynthetic Gene Cluster Reveals a Promising Approach for Identifying New Chemical Scaffolds. <i>MBio</i> , 2020, 11, .	4.1	12
95	Coupling Fluorescence-Activated Cell Sorting and Targeted Analysis of Histone Modification Profiles in Primary Human Leukocytes. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2526-2534.	2.8	9
96	<i>In vitro</i> -Constructed Ribosomes Enable Multi-site Incorporation of Noncanonical Amino Acids into Proteins. <i>Biochemistry</i> , 2021, 60, 161-169.	2.5	9
97	Reducing protein oxidation in low-flow electrospray enables deeper investigation of proteoforms by top down proteomics. <i>EuPA Open Proteomics</i> , 2015, 8, 40-47.	2.5	8
98	Mechanism-Based Small Molecule Cross-Linkers of HECT E3 Ubiquitin Ligase's Substrate Pairs. <i>Biochemistry</i> , 2012, 51, 8327-8329.	2.5	7
99	Reply to "Uveal melanoma cells are resistant to EZH2 inhibition regardless of BAP1 status". <i>Nature Medicine</i> , 2016, 22, 578-579.	30.7	7
100	Development of novel methods for non-canonical myeloma protein analysis with an innovative adaptation of immunofixation electrophoresis, native top-down mass spectrometry, and middle-down <i>de novo</i> sequencing. <i>Clinical Chemistry and Laboratory Medicine</i> , 2021, 59, 653-661.	2.3	7
101	ProSight Annotator: Complete control and customization of protein entries in UniProt XML files. <i>Proteomics</i> , 2022, 22, e2100209.	2.2	6
102	Characterization of a Copper-Chelating Natural Product from the Methanotroph <i>Methylosinus</i> sp. LW3. <i>Biochemistry</i> , 2021, 60, 2845-2850.	2.5	5
103	Stability of histone post-translational modifications in samples derived from liver tissue and primary hepatic cells. <i>PLoS ONE</i> , 2018, 13, e0203351.	2.5	4
104	Chemical composition of material extractives influences microbial growth and dynamics on wetted wood materials. <i>Scientific Reports</i> , 2020, 10, 14500.	3.3	4
105	Biotin Identification Proteomics in Three-Dimensional Organotypic Human Skin Cultures. <i>Methods in Molecular Biology</i> , 2019, 2109, 185-197.	0.9	3
106	Targeted detection and quantitation of histone modifications from 1,000 cells. <i>PLoS ONE</i> , 2020, 15, e0240829.	2.5	3
107	The unique biomineralization transcriptome and proteome of <i>Lytechinus variegatus</i> teeth. <i>Connective Tissue Research</i> , 2018, 59, 20-29.	2.3	2
108	Identification of <i>Plasmodium falciparum</i> proteoforms from liver stage models. <i>Malaria Journal</i> , 2020, 19, 10.	2.3	2

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109	BAP1 Loss Results in EZH2-Dependent Transformation in Myelodysplastic Syndromes. Blood, 2015, 126, 713-713.	1.4	0
110	Therapeutic Targeting of the Histone Ubiquitination-Methylation Axis in T Cell Leukemia. Blood, 2016, 128, 1532-1532.	1.4	0
111	High-Throughput Natural Products Discovery in Fungi Using FACMS Technology. FASEB Journal, 2017, 31, 766.6.	0.5	0
112	Proteome-Selective Imaging of Tissues Using Mass Spectrometry. Angewandte Chemie, 0, , .	2.0	0
113	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
114	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
115	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
116	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
117	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
118	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
119	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
120	Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.		0
121	Innenr¼cktitelbild: Proteome-Selective Imaging of Tissues Using Mass Spectrometry (Angew. Chem.) Tj ETQq1,1 0.784314 rgBT 2,0 0		0